

# Hierarchical Bayes models for Perfusion Imaging

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Interest in imaging blood perfusion *in vivo*

Detection and quantification of areas with pathological high or low blood flow

Applications:

- Oncology (DCE-MRI)
- Ischemic diseases (strokes, DSC-MRI, myocardial)
- Rheumatology



MRI allows non-invasive in-vivo imaging

Imaging of magnetic properties

→ use magnetic contrast agent (CA)

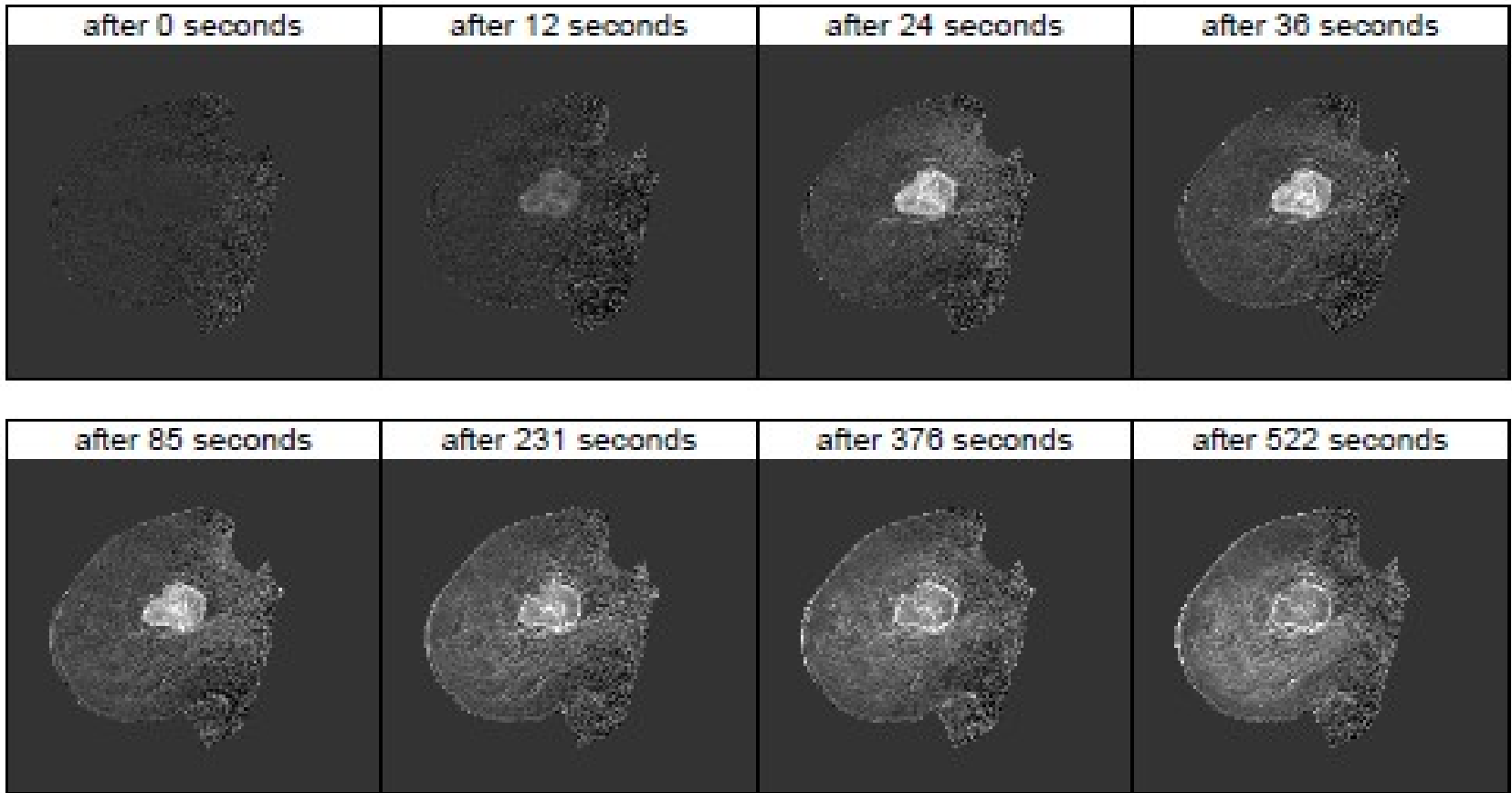
CA travels via blood stream, allows to assess perfusion into tissue

E.g. in oncology (DCE-MRI):

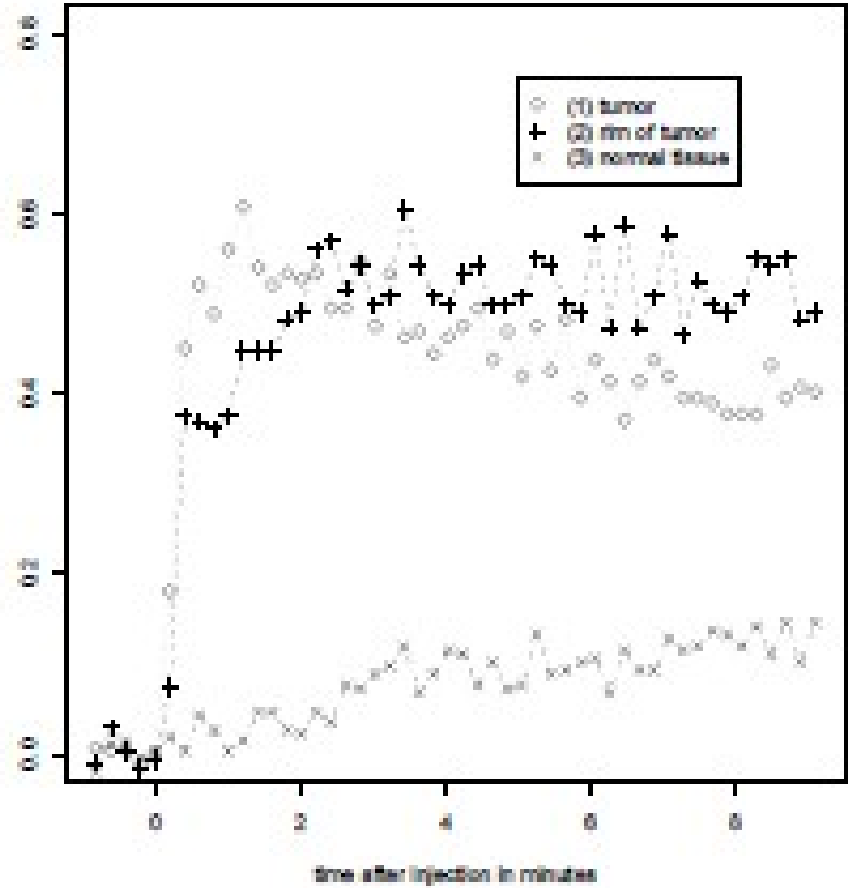
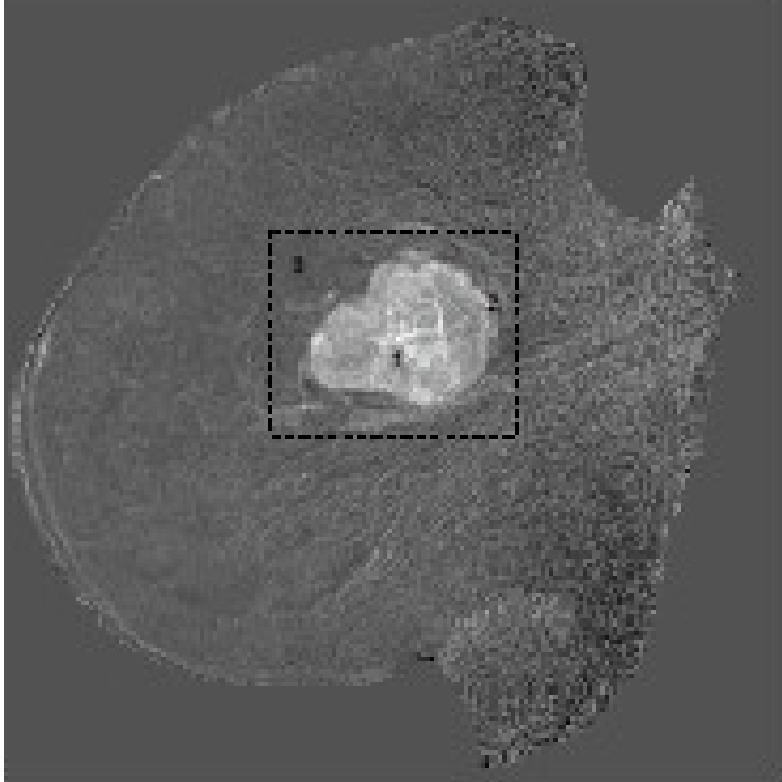
- Angiogenesis: Growth of vessels from cancerous tissue
- Detection/Size measurement
- Diagnostics
- Evaluation of therapy



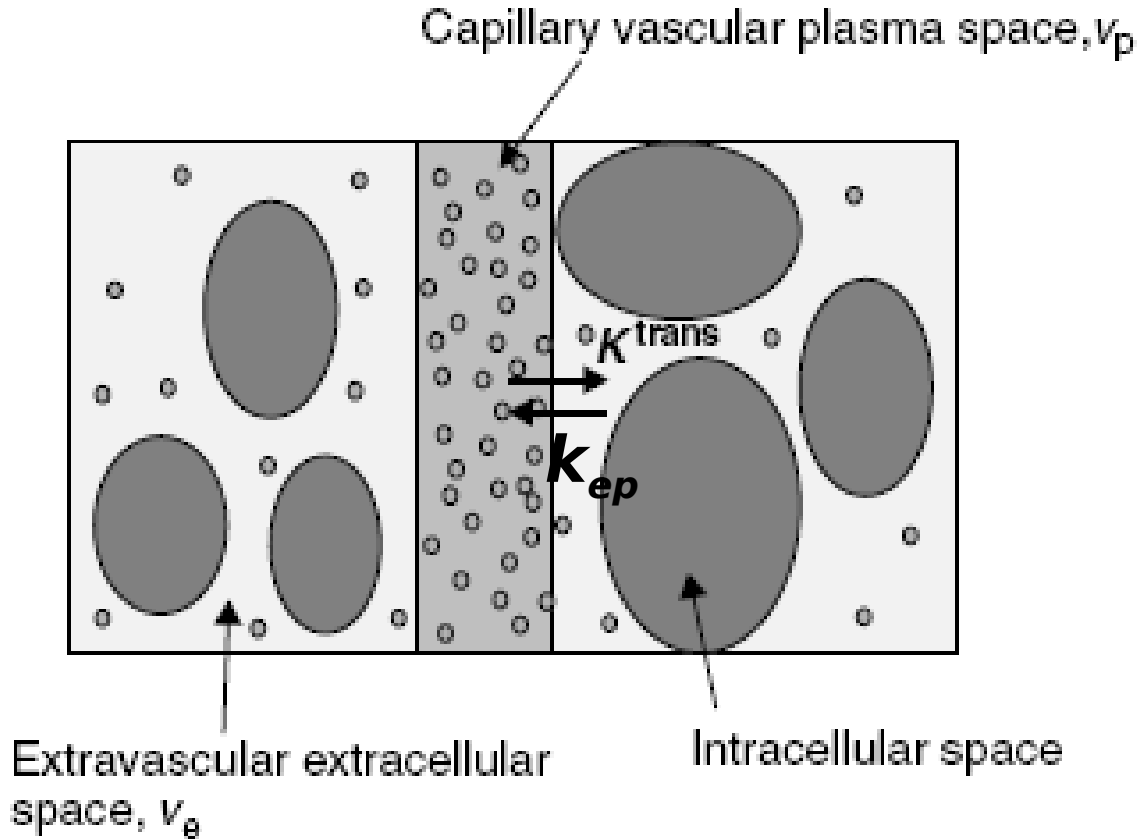
## DCE-MRI - Data



# DCE-MRI - data



# Compartment Model for DCE-MRI



$$C_t(t) = C_p(t) \left( 1 - \frac{v_p}{v_e} \right) + \frac{v_p}{v_e} \int_0^t C_p(u) \exp(-k_{ep}(t-u)) du$$

# Myocardial Perfusion

$$S(t) = A(t) \otimes f(t)$$

$A(t)$  measured in left ventricle blood pool

$$S = \mathbf{A}f = \mathbf{A}\mathbf{B}\beta = D\beta$$

Jerosch-Herold et al. (IEEE TMI 2004)

Response  $f$  modeled as penalized B-Spline

$$f(t) = \sum_{p=1}^P B_{pt} \beta_p \quad \beta_{ip} \sim \mathbf{N}(\beta_{i,p-1}, \lambda^2)$$

Schmid (IEEE TMI 2011)

## Other local models

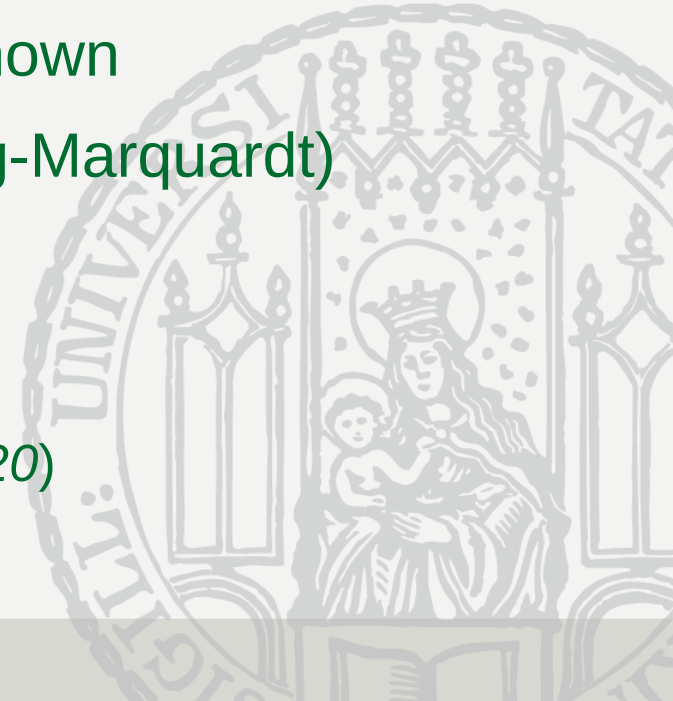
- Linear Models → fMRI (e.g., Brezger, Fahrmeir, Hennerfeind 2009 JRSS)
- Two-, N-compartment models
  - Model choice
  - See Kaercher, Schmid, ISBI 2010)
- Stochastic differential equations (for FRAP)
  - See Dargatz, 2010



- Model for breast cancer

$$C_t(t) = DK^{trans} \sum_{i=1}^2 \frac{a_i (\exp(-m_i t) - \exp(k_{ep} t))}{k_{ep} - m_i}$$

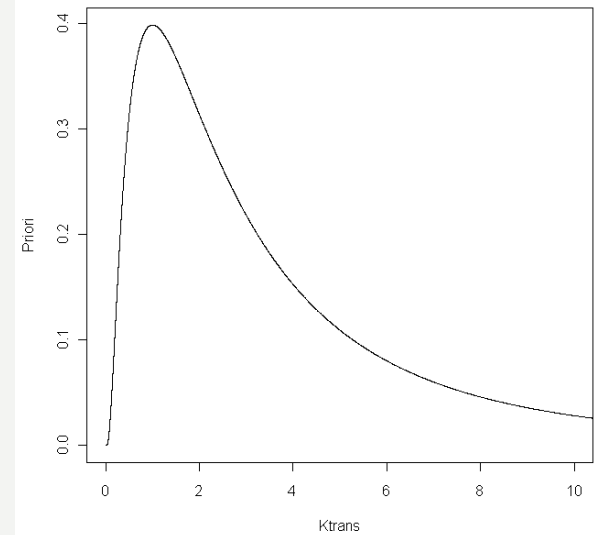
- AIF parameters  $D$ ,  $a_1$ ,  $a_2$ ,  $m_1$ ,  $m_2$  known
- Least square algorithm (Levenberg-Marquardt)
  - Starting values?
  - Convergence?
  - Biological not realistic values ( $K^{trans} > 20$ )



Use Priori-Information:

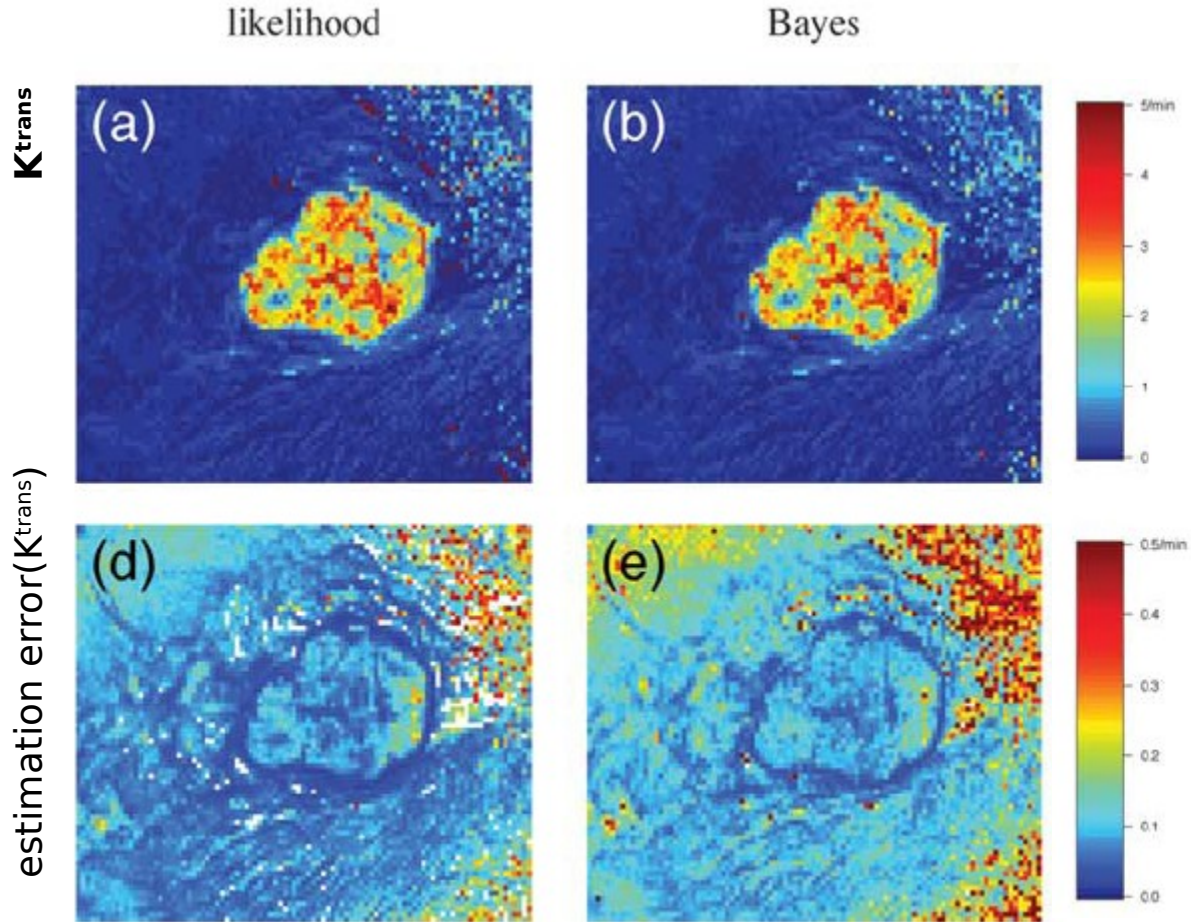
$$\theta = \log(K^{\text{trans}}) \sim N(0,1)$$

$$\phi = \log(k_{\text{ep}}) \sim N(0,1)$$



$$p(K^{\text{trans}}, k_{\text{ep}} | Y) = \frac{l(Y) p(K^{\text{trans}}, k_{\text{ep}})}{\int l(y) p(h) dh}$$

# Parameter maps



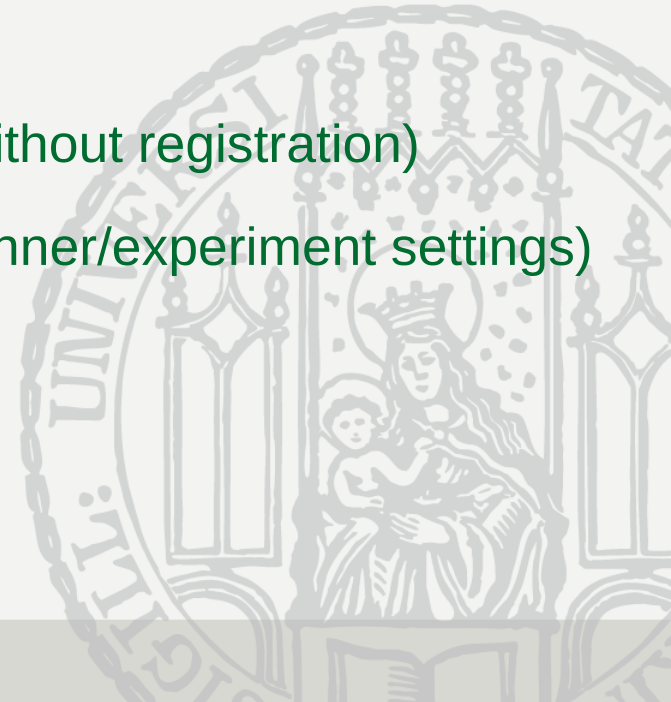
# Contextual information

- Although models are simplified, model fitting is typically challenging
  - “Very non-linear”
  - Low signal-to-noise ratio
  - Convolution
- Use contextual information to make model fitting more robust (“borrowing strength”)
- Use contextual model to test dependencies



# Contextual information

- Spatial information, inherent in images
  - Adjacent voxels share same tissue, have similar properties
  - Voxel grid is arbitrary
  - But: account for edges, sharp features
- Meta information
  - Images from same object (with or without registration)
  - Covariates (patient information, scanner/experiment settings)
  - Additional observations (e.g. EEG)



Level 1: Noise structure

Level 2: Local model (Kinetics)

Level 3: Contextual information (e.g., spatial)

Level 4: Hyper parameters (e.g., smoothing parameters)

- Prior information on latent, unobserved parameters
- “Flat priors”



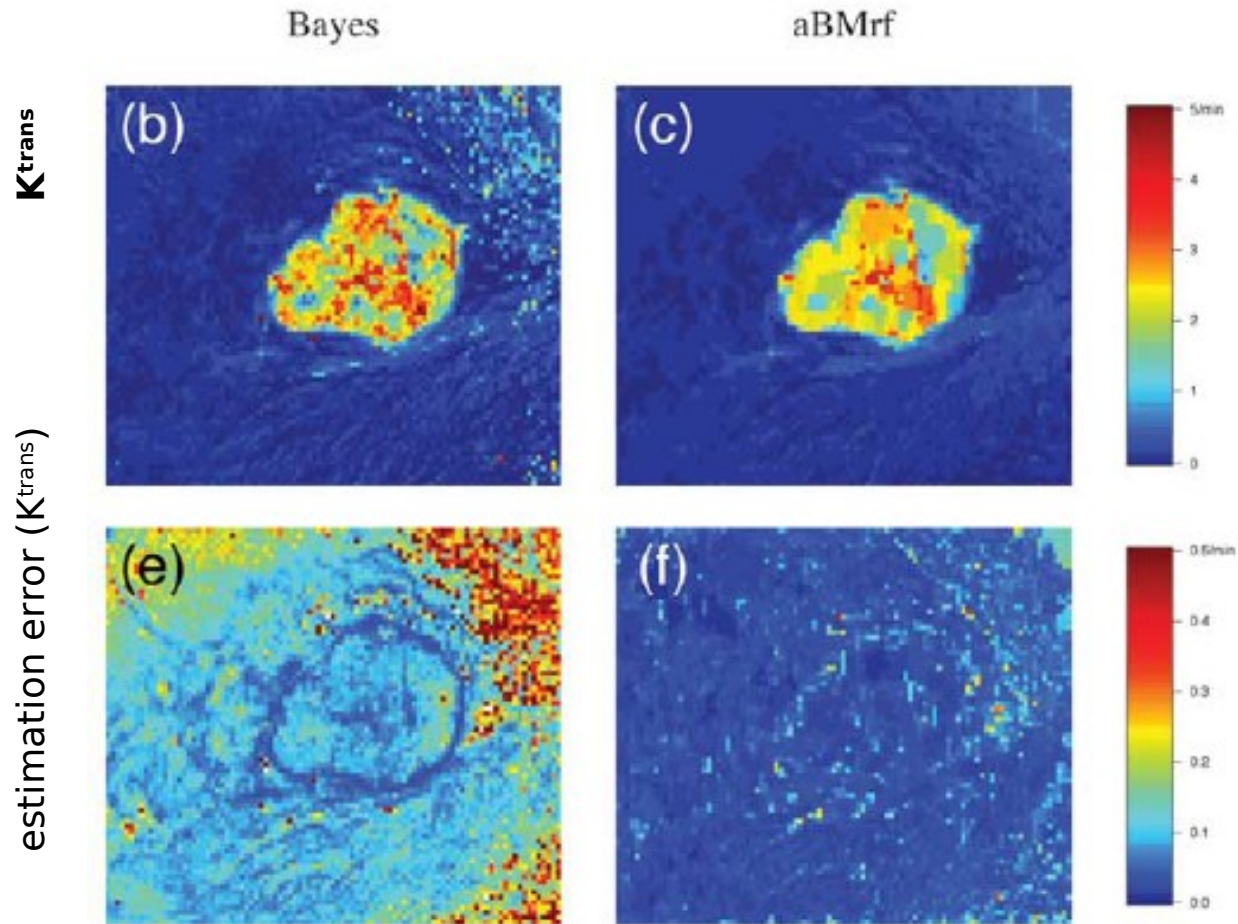
# Markov random field for DCE-MRI

- Assumption: Adjacent voxel have similar kinetic parameters
- Markov random field on  $K^{trans}$  and  $k_{ep}$

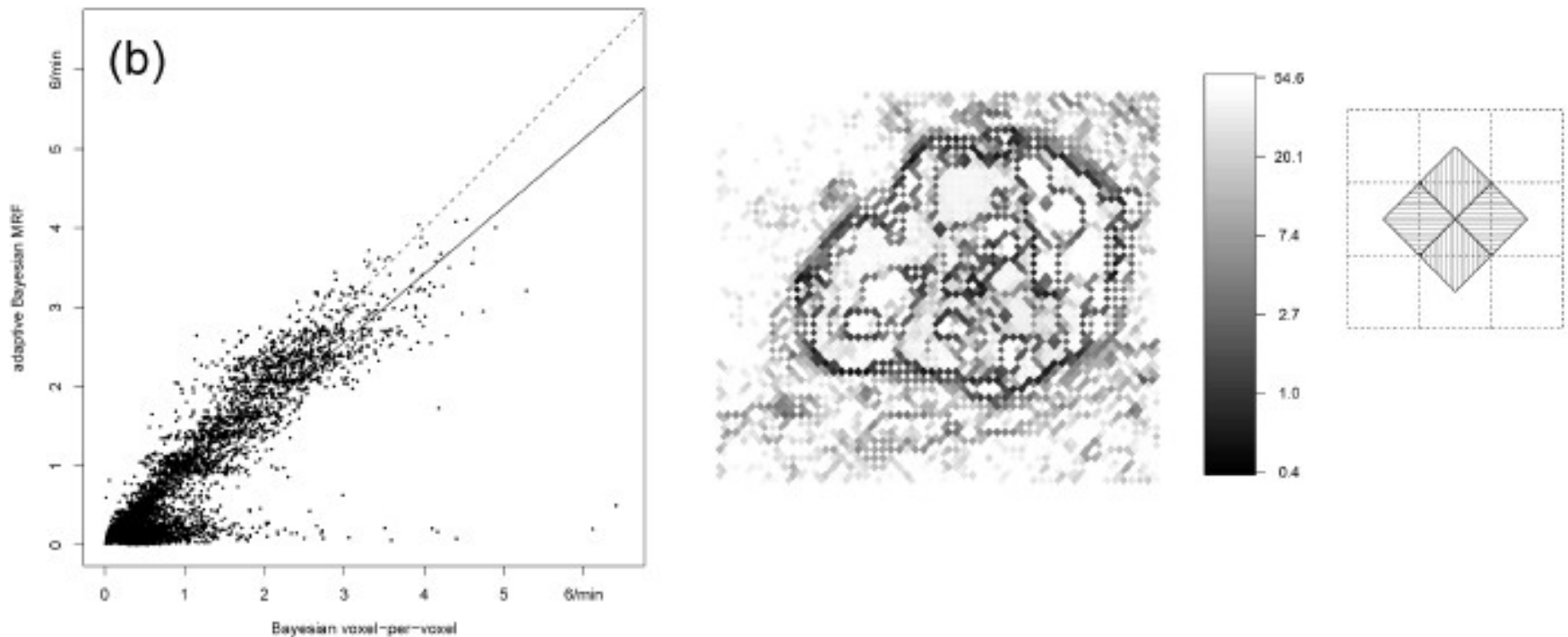
$$\log(K_i^{trans}) \sim N\left(\sum_{j \in \partial_i} w_{ij} \log(K_j^{trans}), 1 / \sum_{j \in \partial_i} w_{ij}\right)$$

- Spatial smoothing has to account for edges and sharp features
- Smoothing weights  $w_{ij}$  are estimated locally and adaptively from the data

# Results spatial DCE-MRI



## Results spatial DCE-MRI



Schmid, Witcher, Padhani, Taylor, Yang, IEEE TMI (2006), 25:12, 1627-1636

- In longitudinal drug studies, we are interested in finding differences in the 4D images
- For example, anti-angiogenesis drugs should lower  $K^{\text{trans}}$  values
- Standard procedure:
  - Estimate  $K^{\text{trans}}$
  - Compute average  $K^{\text{trans}}$  per scan
  - Test on differences between groups
- Low patient numbers
- Information loss by averaging

Patient ID	Pre	post
1	0.208	0.161
2	0.355	0.120
3	0.255	0.031
4	0.230	0.245
5	0.199	0.208
6	0.154	0.173
7	0.264	0.327
8	0.198	0.223
9	0.305	0.122
10	0.267	0.221
11	0.432	0.111
12	0.174	0.113

Voxels are from a scan

Scans are from a patient

Patient has some response to treatment and has certain properties (covariates  $z$ )

→ Use mixed effect model as contextual information

$$\log(K_{is}^{trans}) = \alpha^T z + \beta x_s + \gamma_i + \delta_i x_s + \varepsilon_{is}$$

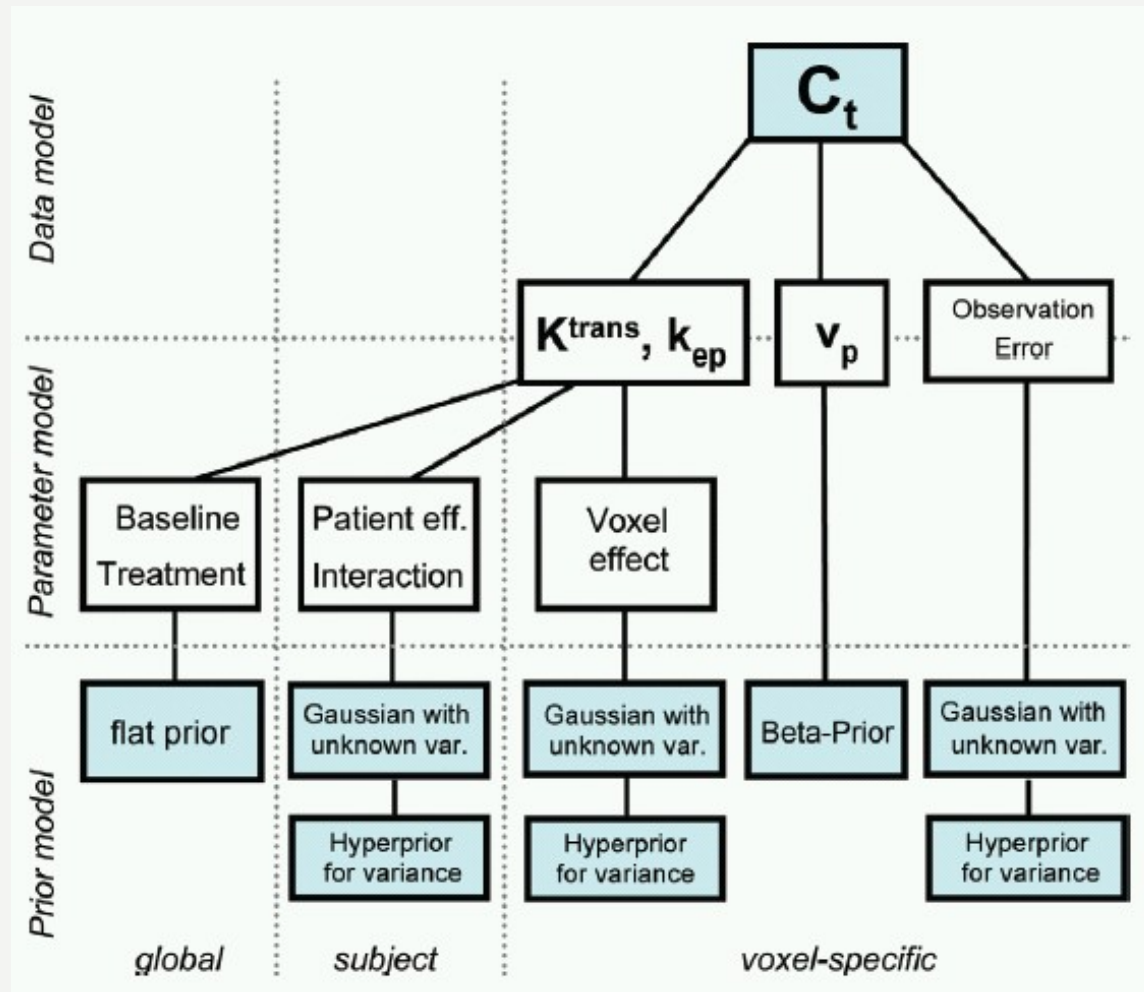
$\alpha, \beta$  fixed effects;  $\gamma, \delta, \varepsilon$  random effects

Observed data

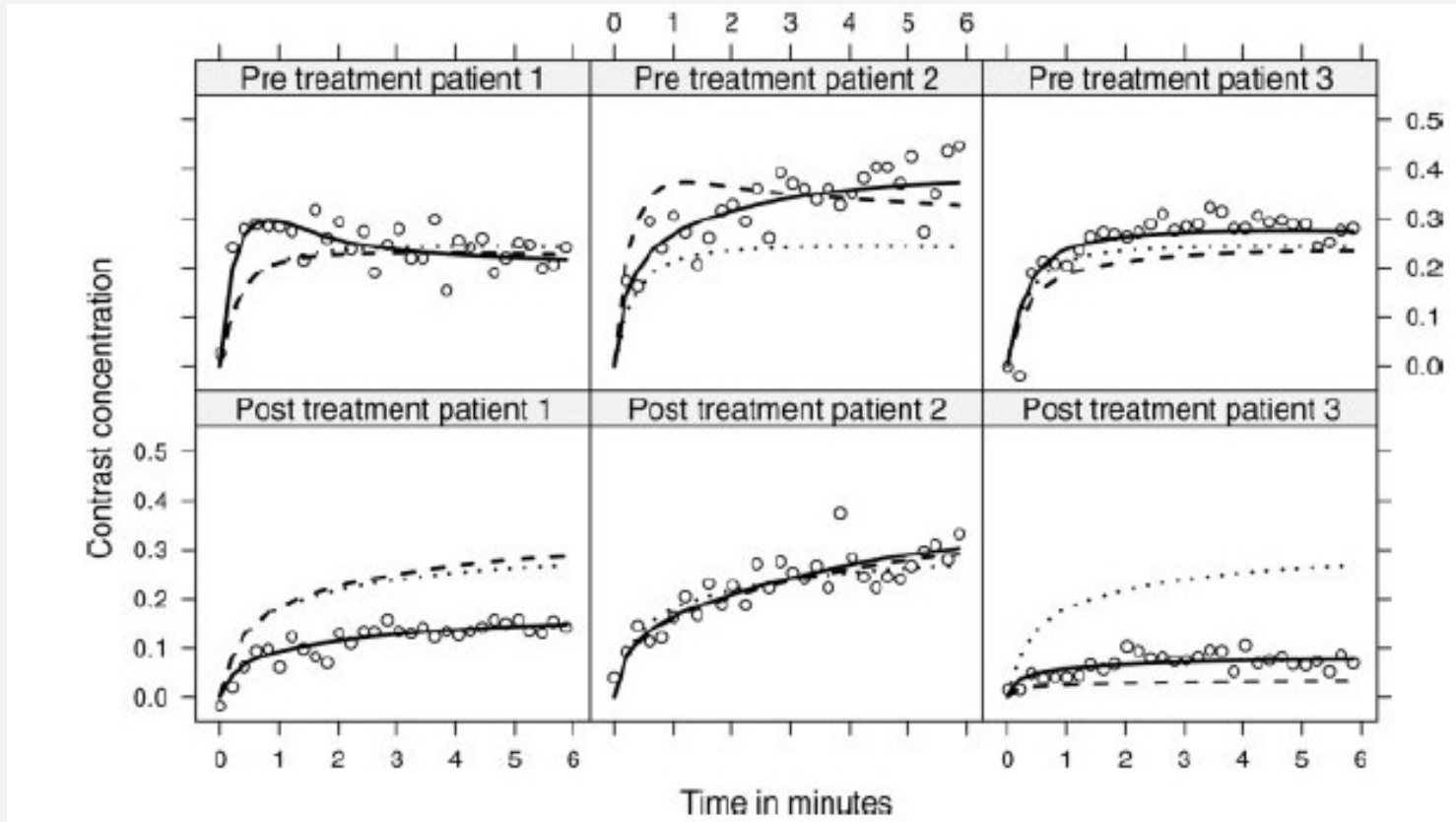
Local kinetic model

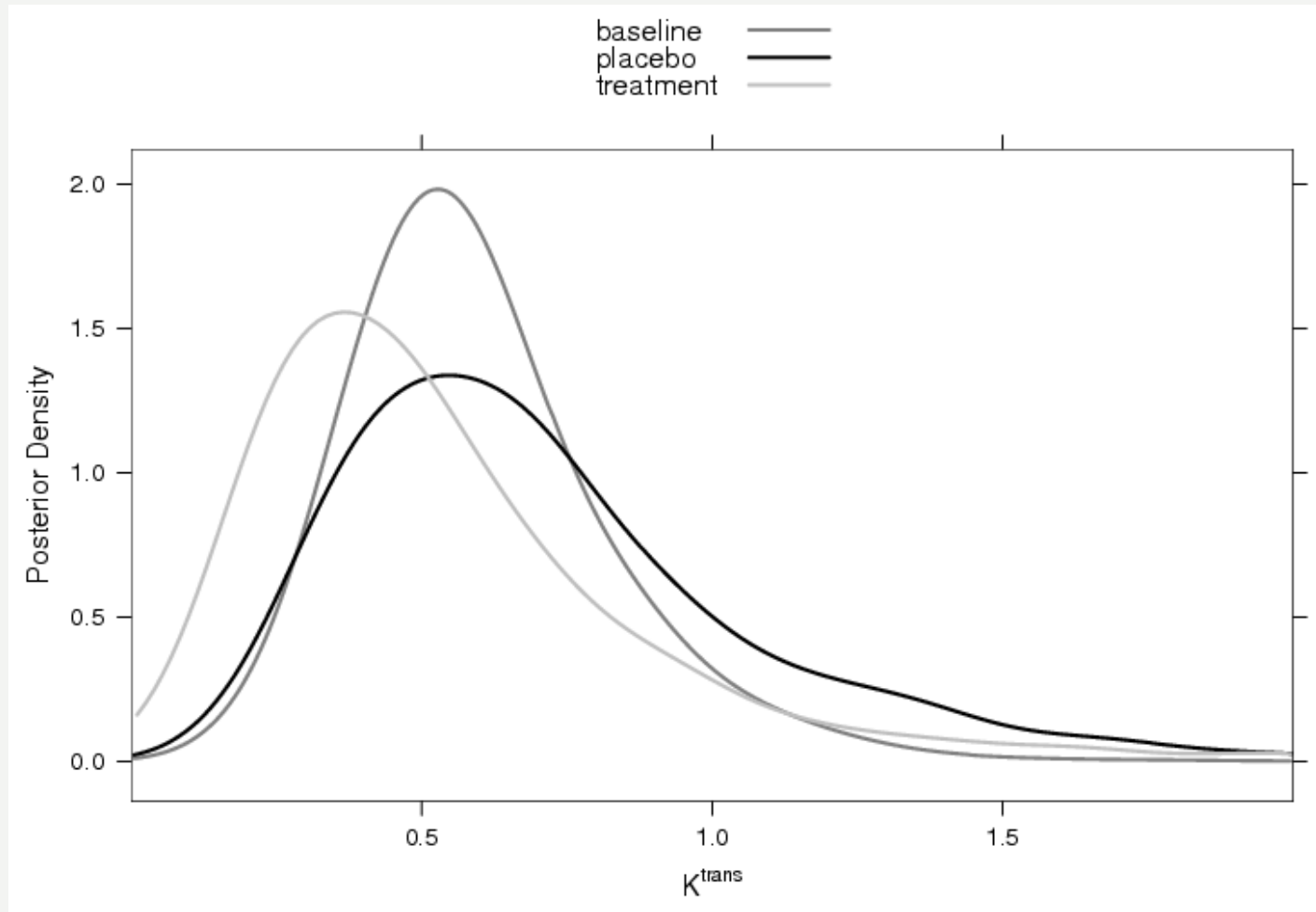
Context (study model)

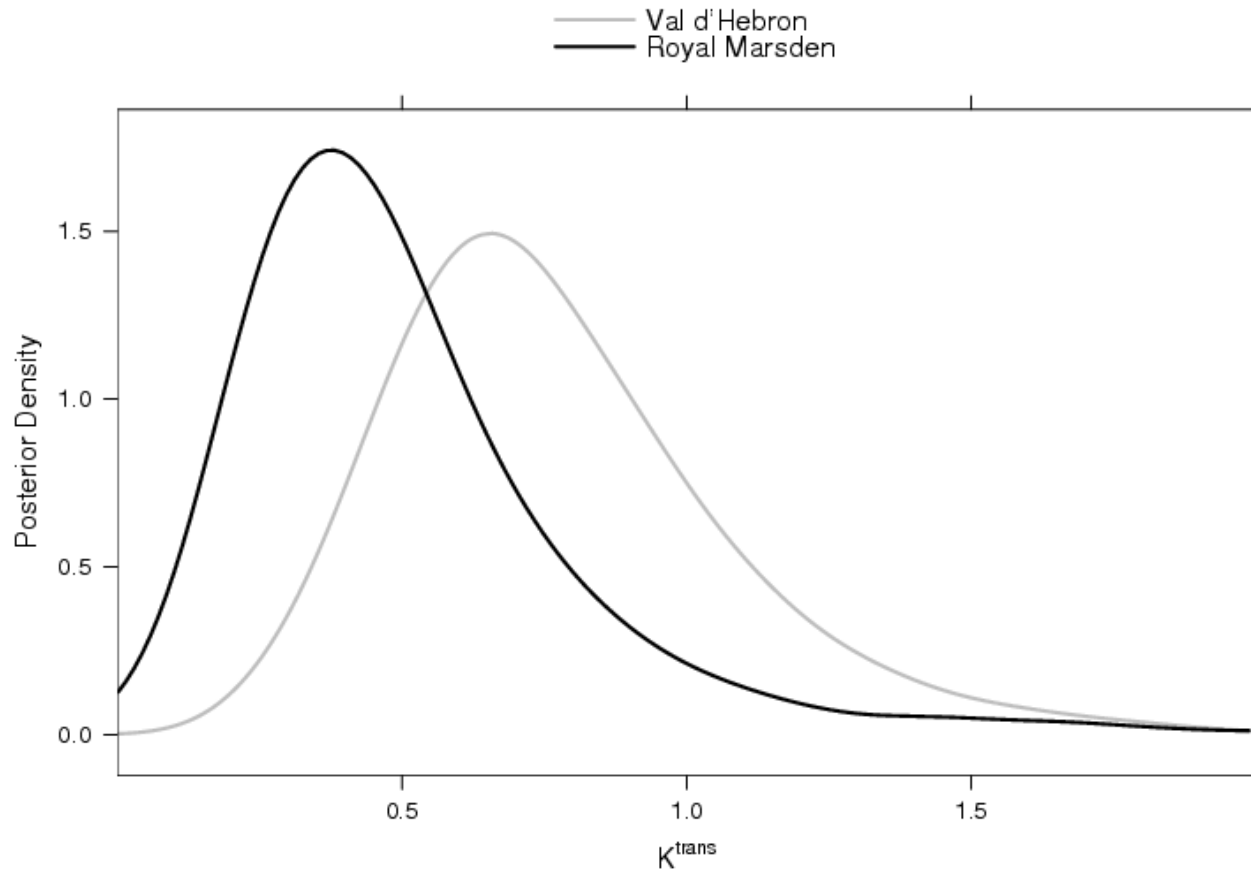
Prior information



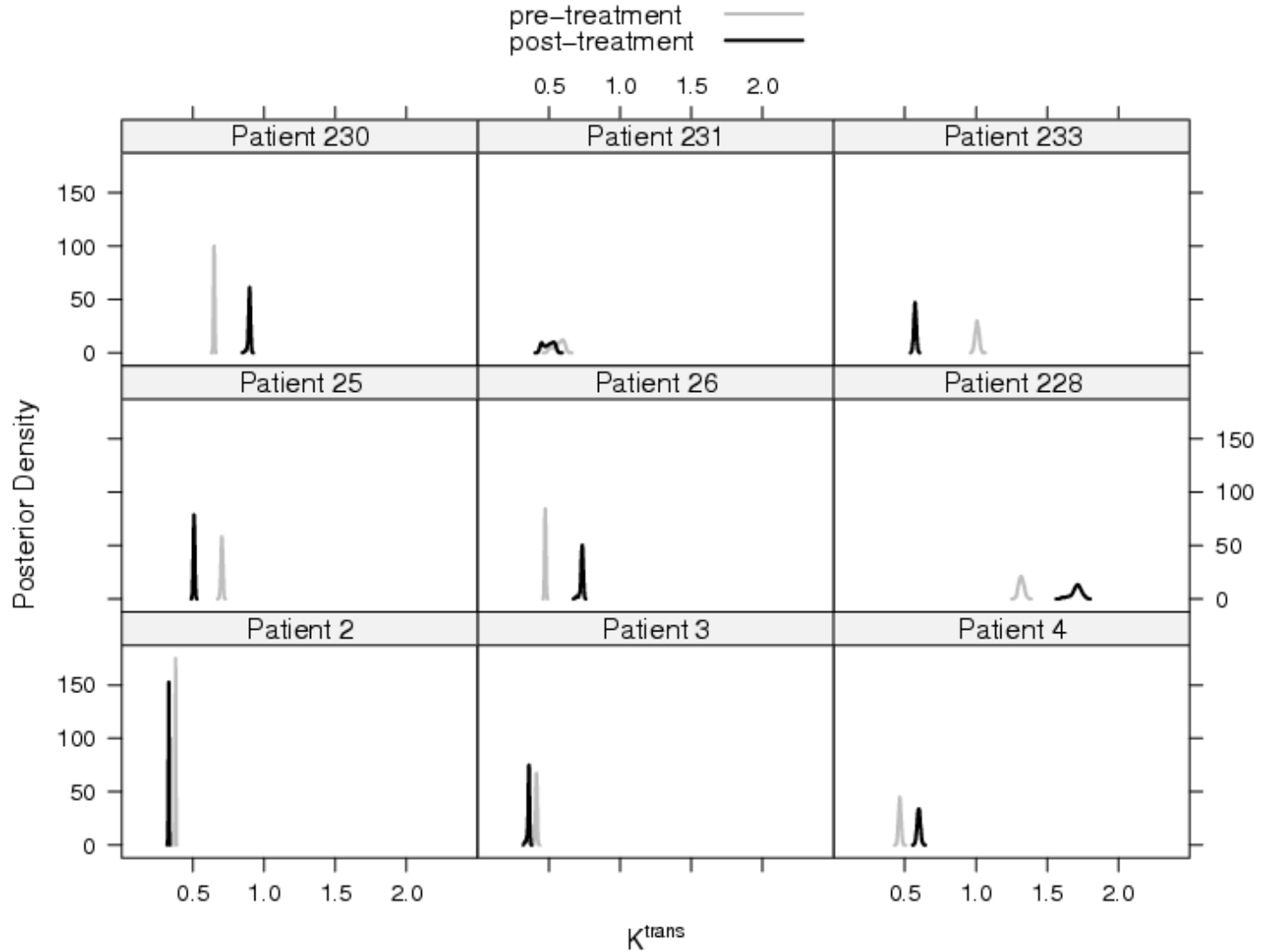
# Mixed effect time curves



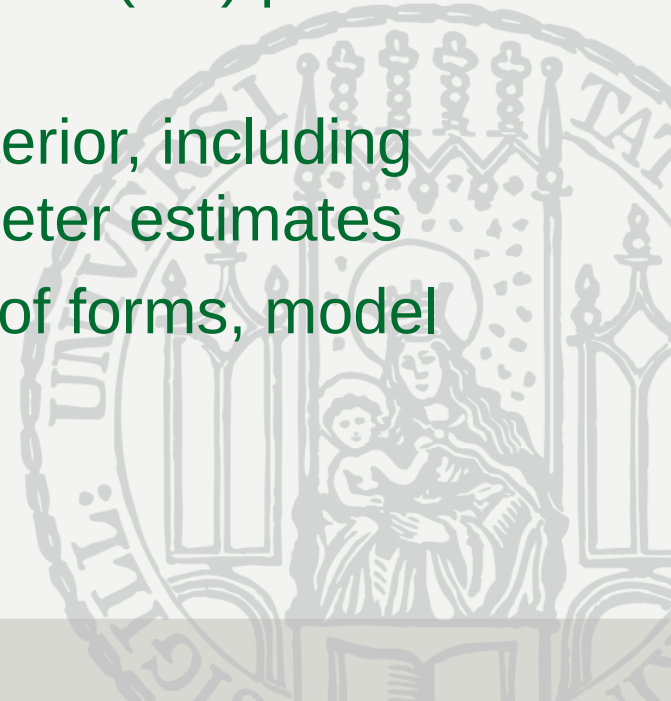




# Results LoMIS



- We use contextual information to
  - Gain strength for local model fitting
  - Gain information on dependencies (allows tests)
- Contextual information is defined via (flat) prior distributions
- Conclusions are drawn from posterior, including uncertainty information on parameter estimates
- Local models can have a variety of forms, model choice (?)



Thanks for your attention!

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